

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:21:43 ; Search time 2513 Seconds

(without alignments)
16625.306 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccgaatttga.....aatctccgtataaaaatt 1719

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estb1:*
2: em_estb2:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	532.2	31.0	537	9 AW783013	AW783013 ra22d01.y
2	511.8	29.8	556	10 BE239174	BE239174 MD0830 Me
3	320.8	18.7	650	9 AW152739	AW152739 JALSL3C10
4	301.4	17.5	327	9 AW589077	AW589077 ra08c01.y

ALIGNMENTS

RESULT 1
AW783013
LOCUS ra22d01.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
DEFINITION CDNA 5' similar to WP:F57B10.3 CELL302 PHOSPHOGLYCERATE MUTASE ;
mRNA sequence.
ACCESSION AW783013
VERSION AW783013.1 GI:7797619
KEYWORDS EST.
SOURCE Meloidogyne incognita
ORGANISM Meloidogyne incognita
REFERENCE 1 (Bases 1 to 537)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvill,I., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

5 300.8 17.5 677 12 BJ112231
6 292.6 17.0 655 9 AU204921
7 290.6 16.9 652 12 BJ121936
8 287.6 16.7 649 10 BJ108160
9 283 16.5 647 14 CB374256
10 278.2 16.2 285 13 BQ613449
11 277.2 16.1 580 12 BJ116367
12 272.8 15.9 623 12 BJ107746
13 271.4 15.8 620 12 BJ107756
14 270.6 15.7 726 12 BJ155870
15 269.8 15.7 621 12 BJ117851
16 269.2 15.7 623 12 BJ125855
17 269.2 15.7 651 12 BJ126726
18 261.8 15.2 584 12 BJ124149
19 261.8 15.2 585 12 BJ113563
20 261.8 15.2 596 12 BJ101770
21 260.2 15.1 544 12 BJ120572
22 259.8 15.1 621 10 BF423140
23 258.2 15.0 557 9 AU207271
24 257.4 15.0 592 9 AU205988
25 255.6 14.9 686 14 CB013135
26 246.2 14.3 791 12 BJ154227
27 241 14.0 700 9 AA629457
28 240.4 14.0 552 12 BJ109590
29 238.2 13.9 521 14 M88904
30 237.2 13.8 759 12 BJ148082
31 230.2 13.4 471 12 BI773091
32 229.8 13.4 748 12 BJ141355
33 225.2 13.1 561 12 BJ103886
34 224.6 13.1 476 9 AA273165
35 224.4 13.1 745 12 BJ150141
36 224.2 13.0 506 9 AI065990
37 224.2 13.0 561 9 AU208103
38 223.6 13.0 764 9 AW332502
39 222.8 13.0 736 12 BJ149541
40 222.8 13.0 739 12 BJ148716
41 220.4 12.8 602 12 BI174231
42 220.2 12.8 546 14 CB403894
43 220 12.8 557 10 BE899657
44 219.6 12.8 607 9 AU222303
45 219.2 12.8 542 9 AU209097

537 bp mRNA linear EST 10-MAY-2001
ra22d01.y1 Bird-Rao Meloidogyne incognita J2 Meloidogyne incognita
CDNA 5' similar to WP:F57B10.3 CELL302 PHOSPHOGLYCERATE MUTASE ;
mRNA sequence.
ACCESSION AW783013
VERSION AW783013.1 GI:7797619
KEYWORDS EST.
SOURCE Meloidogyne incognita
ORGANISM Meloidogyne incognita
REFERENCE 1 (Bases 1 to 537)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarisvill,I., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

BJ112231 BJ112231
AU204921 AU204921
BJ121936 BJ121936
BJ108160 BJ108160
CB374256 CB374256
BQ613449 BQ613449
BJ116367 BJ116367
BJ107746 BJ107746
BJ107756 BJ107756
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BJ149541 BJ149541
BJ148716 BJ148716
BI174231 BI174231
CB403894 CB403894
BE899657 BE899657
AU222303 AU222303
AU209097 AU209097

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

The library was constructed by Uma Rao and David Bird
(david_bird@ncsu.edu) at North Carolina State University. DNA
Sequencing by: Washington University Genome Sequencing Center St.
Louis.

Seq primer: T3 ET from Amerham
High quality sequence stop: 419.

FEATURES

source

1. 537
Location/Qualifiers

/organism="Meloiodogyne incognita"

/mol_type="mRNA"

/db_xref="taxon:6306"

/dev_stage="enriched for 2nd stage juveniles"

/lab_host="XLOL"

/clone_lib="Bird-Rao Meloiodogyne incognita J2"

/note="Vector: ZAP express - pBRCMV (Stratagene); Site 1:
EcoRI; Site 2: XhoI; Oligo (dT) primed library. cDNA was
constructed and cloned unidirectionally into the vector
within the 5' EcoRI and 3' XhoI sites. This library was
constructed by Dr. Uma Rao and Dr. David Bird at North
Carolina State University."

BASE COUNT 152 a 92 c 123 g 170 t

ORIGIN

Query Match 31.0%; Score 532.2; DB 9; Length 537;

Best Local Similarity 99.4%; Pred. No. 1.2e-118;

Matches 534; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 580 ACTGGACGTTATTATCAATGGATGGGACAAAGATGGGCGTATTAAAGATGGCTTAT 639

Db 1 ACTGGACGTTATTATCAATGGATGGGACAAAGATGGGCGTATTAAAGATGGCTTAT 60

QY 640 GAGGCAATTTGGAGGATTATGGACAAAAGCCAGCTGTATGAAGCTGTGATGTGTT 699

Db 61 GAGGCAATTTGGAGGATTATGGACAAAAGCCAGCTGTATGAAGCTGTGATGTGTT 120

QY 700 AGAGACGATATGCTCAATCTGAGACTGACGATTTCTGAACCAATTTCTTTTCGGAC 759

Db 121 AGAGACGATATGCTCAATCTGAGACTGACGATTTCTGAACCAATTTCTTTTCGGAC 180

QY 760 GATGGCGAGTAAAGATGACGATCTTATTTTCTCAATATGCTGCTGATCGTATG 819

Db 181 GATGGCGAGTAAAGATGACGATCTTATTTTCTCAATATGCTGCTGATCGTATG 240

QY 820 CGTCAATTTGTGAATTTGGTCTCGACGTTATGAAGCTTAAAGATCTTAATAGTTCGGTTCCT 879

Db 241 CGTCAATTTGTGAATTTGGTCTCGACGTTATGAAGCTTAAAGATCTTAATAGTTCGGTTCCT 300

QY 880 CACCCTAAATATTCAGATTAGTGGATGACCCATACAAATGAAGAGTTTCCATTCCA 939

Db 301 CACCCTAAATATTCAGATTAGTGGATGACCCATACAAATGAAGAGTTTCCATTCCA 360

QY 940 TCGTTATCCCACTGTGACTCATATAATGTGCTGCTGAATGGCTTCTCTCAAGGA 999

Db 361 TCGTTATCCCACTGTGACTCATATAATGTGCTGCTGAATGGCTTCTCTCAAGGA 420

QY 1000 GTTACTCAATTTCACTGTGCGGAACTGAGAAGTATCCTCATGTTACCTTCTCTTTAAT 1059

Db 421 GTTACTCAATTTCACTGTGCGGAACTGAGAAGTATCCTCATGTTACCTTCTCTTTAAT 480

QY 1060 GGTGGTCGAGAAGTTCAATTTCCAAGATGAAGAGCGTTGTATGTTCCGTCACCAAAA 1116

Db 481 GGTGGTCGAGAAGTTCAATTTCCAAGATGAAGAGCGTTGTATGTTACGTCATCAAGA 537

RESULT 2

BE239174

LOCUS

MD0830 Meloiodogyne incognita J2 (#MD99-1) linear EST 11-JUL-2000

DEFINITION cDNA clone 3739 5' similar to phosphoglycerate mutase (AF039713),

mRNA sequence.

ACCESSION

BE239174

VERSION BE239174.1 GI:9034138

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Meloiodogyne incognita (southern root-knot nematode);

Meloiodogyne incognita

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Meloiodogyninae; Meloiodogyne.

1 (bases 1 to 556)

Dautova, M., Gommers, F.J., Bakker, J. and Smant, G.

5' end expressed sequence tags from Meloiodogyne incognita

preparasitic J2 cDNA library

Unpublished (2000)

Contact: Smant G / Dautova M

Laboratory of Nematology

Wageningen University and Research Center

Box 8123, Binnenhaven 10, 6709 PD Wageningen, The Netherlands

Tel: 31 317 485 254

Fax: 31 317 484 254

Email: Geert.Smant@medew.nema.wau.nl,

Makedonka.Dautova@medew.nema.wau.nl

Insert Length: 556 Std Error: 0.00

Seq primer: T7 promoter primer

High quality sequence stop: 556.

Location/Qualifiers

1. 556

/organism="Meloiodogyne incognita"

/mol_type="mRNA"

/db_xref="taxon:6306"

/clone="3739"

/dev_stage="second stage parasitic juveniles (J2)"

/note="Vector: pMAK1; Site 1: Sfi IA; Site 2: Sfi IB; cDNA

was synthesized using SMART III oligo, CDS III oligo d(T

30 (Clontech) and Superscript II reverse transcriptase

(Life Technology). cDNA clones were size fractionated and

directionally ligated in the Sfi IA restriction site at

5' end and Sfi IB at 3' end of pMAK1. pMAK1 was derived

from the plasmid pcDNA II (Invitrogen)."

BASE COUNT 161 a 113 c 124 g 158 t

ORIGIN

Query Match 29.8%; Score 511.8; DB 10; Length 556;

Best Local Similarity 99.1%; Pred. No. 1.1e-113;

Matches 546; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

QY 994 CAAGGAGTTACTCAATTTCACTGTGCGGAACTGAGAACTATCCTCATGTTACCTTCTTC 1053

Db 9 CAAGGAGTTACTCAATTTCACTGTGCGGAACTGAGAACTATCCTCATGTTACCTTCTTC 68

QY 1054 TTTAATGGTGGTCGAGAAGTTCAATTCAGATGAAGAGCGTTGTATGTTCCGTCACCA 1113

Db 69 TTTAATGGTGGTCGAGAAGTTCAATTCAGATGAAGAGCG-TGTATGTTCCGTCACCA 127

QY 1114 AAAGAAGTTGCTACATATGATTTAAACCCAGAAATGAATGCTGCTGGAGTTGCCGAAAAA 1173

Db 128 AAAGAAGTTGCTACATATGATTTAAACCCAGAAATGAATGCTGCTGGAGTTGCCGAAAAA 187

QY 1174 ATGGTCGAGCAATTTGAGTCAGGAGGATCCTTTGGTTATGTGCAATTTTGGCGCTCTCT 1233

Db 188 ATGGTCGAGCAATTTGAGTCAGGAGGATCCTTTGGTTATGTGCAATTTTGGCGCTCTCT 247

QY 1234 GACATGGTTGGACATCTGGTAAATTTGAACCTGCGCTCAAAAGCATGTCAAGCTACTGAC 1293

Db 248 GACATGGTTGGACATCTGGTAAATTTGAACCTGCGCTCAAAAGCATGTCAAGCTACTGAC 307

QY 1294 GAGGCAATTTGGAAGATATTTGAAGCATGCCAAACTTATAAATACGTTCTTATGGTTACT 1353

Db 308 GAGGCAATTTGGAAGATATTTGAAGCATGCCAAACTTATAAATACGTTCTTATGGTTACT 367

QY 1354 TCCGATCATGGAATGCTGAGAGAGATGATGCTCCCGATGGTAGTGAACATACTGCACAT 1413

Db 368 TCCGATCATGGAATGCTGAGAGAGATGATGCTCCCGATGGTAGTGAACATACTGCACAT 427

Caenorhabditis elegans cDNA clone yk843c10 5', mRNA sequence.

AU204921
VERSION AU204921.1 GI:14836754
KEYWORDS EST.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea
AUTHORS ; Rhabditiidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 655)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y,
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished
Contact: Yuji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel.: 81-559-81-6854
Fax: 81-559-81-6855
Email: yokohar@lab.nig.ac.jp.

FEATURES
source Location/Qualifiers
1..655
 ~~/organism="Caenorhabditis elegans"~~
 ~~/mol_type="mRNA"~~
 ~~/strain="N2"~~
 ~~/db_xref="taxon:6239"~~
 ~~/clone="yk843c10"~~
 ~~/sex="Hermaphrodite"~~
 ~~/tissue_type="whole animal"~~
 ~~/dev_stage="L4"~~
 ~~/clone_lib="unpublished oligo-capped cDNA library, stage L4"~~

BASE COUNT	175 a	124 c	169 g	187 t
Query Match	17.08;	Score 292.6;	DB 9;	Length 655;
Best Local Similarity	67.6%;	Pred. No. 3e-60;	Mismatches 201;	Indels 3;
Gaps 1;				
Matches 425;				
Qy	17	TTGAGATGGACAATAATCAAAATCTTCCACAAAAGTCGTCTGTGTAGTTTGATTTGCATGGAT	76	
Db	27	TGGCGATTGGCAATATACAGTTCGGTGCCCAATAGGTCTGTCTCATCGTTATTGATGGAT	86	
Qy	77	GGGGCCTTTCGGATGAACACACAGCGGAATGCAATTGTCAAAGCTAAAAACGCCCTATTATGG	136	
Db	87	GGGGAGTTCTGAAGATCCITTACGGTAACGCTATTCTCAACGCACACACCACCTATTATGG	145	
Qy	137	ACAACTTTGTTCTGGAAATTTGGCAAAATTTGGAAGCACACAGGTCCTTCATGTTGGATTGC	196	
Db	147	ACAAGCTGTGTCGGGCAATTTGGCTCAAAATTTAGGCACATGGTCTTCATGTTGGTCTCC	206	
Qy	197	CAGAAGCCTTAATGGGAAATCTCGAAGTTGGACATTTTGAATATPAGGAGCTGGGAAGATTGA	256	
Db	207	CAGAAGGATTGATGGGAAATTTGGGAATTCGGACATTTTGAACATCGGACGGAGCTGTTA	266	
Qy	257	TTTTATCAAGATATTGTTCGAATTAAATTTGGCTGTTCACGAAACAGGTTGTTTACAAATC	316	
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Qy	317	CTCAGATTGTCATCAGCTCAGCGTCGAAAGAGGGAGGTGGTFCGATTGCATTTATTAG	376	
Db	327	AGAGCTTGGTGGATGCTTGGCGATCGTGCTAAAAACGGAAATGGACGCTCTCATCTGCGCG	386	
Qy	377	GACTGGTTAGCGATGGTGGTGCCACCTCATATTGATCATCTTTTTTCGGTGTGATAGTG	436	
Db	387	GACTTGTGTTCTGACGGAGGTGTTCATTCTCTCATATTGATCATCTTTTGTGTTAAGG	446	
Qy	437	CATTAAACAATTAACAAGTGCCAAGGTTTTCATTTCTTTTTCGTGATGGTGCGAGATA	496	
Db	447	CCATCAAGAGCTCGGAGTTCCAGAACTTTACCTTCATTTCTACGGAGATGGTCGTGATA	506	
Qy	497	CTTCGCCCAACAAGTGGAGCTGGTTTATCTTGAACAACCTTCTCAATTTATTG -- -CTTCGG	553	

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Db      507 CTCTCCAAACAGTGGAGTTGGATTCTCTTGAAACAAACCCCTCGAGTCTTCTTGGAGAAACTA 566
Qy      554 AAAAGTACGGAGAAATGGCTACTATTACTGGAGCTTATTATGCAATGGATAGGGACAAAA 613
Db      567 CTGGATATGCAAAACTAGCTACTGTAGTTGGCCGCTACTATGCTATGATCGCGATAACA 626
Qy      614 GATGGGAGCGTATTAAAGATGGCTTATGAG 642
Db      627 GATGGGAGCGTATCAATGTTGCATCAG 655

RESULT 7
BJ121936
LOCUS   652 bp mRNA linear EST 23-JAN-2002
DEFINITION
BJ121936 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1282f07 5', mRNA sequence.
ACCESSION
BJ121936
VERSION
BJ121936.1 GI:18282074
KEYWORDS
EST.
SOURCE
Caenorhabditis elegans
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE
1 (bases 1 to 652)
Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.
and Sugano, S.
A complementary view of the C.elegans genome
Unpublished
Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .652
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk1282f07"
/sex="hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L1"
/clone_lib="unpublished oligo-capped cDNA library, C.
elegans L1 stage"
BASE COUNT 173 a 124 c 168 g 187 t
ORIGIN

Query Match 16.9%; Score 290.6; DB 12; Length 652;
Best Local Similarity 67.5%; Pred. No. 9.2e-60;
Matches 423; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

Qy      17 TTGAGATGGGACAATATCAAAATGTTCAACAAAAGTCTGCTGTAGTTATTGATGATGAT 76
Db      26 TGGCGATGGCAATAAACAAGTTCGGTGCCCAATAGGCTCTGCTCATCGTTATGATGAT 85
Qy      77 GGGGCCCTTCGATGAACAACACGGGAATGCAATTGCTAAAGCTAAACGCCTATTATGG 136
Db      86 GGGGAGTTTCTGAAGATCCCTACGGTAACGCTATTCTCAACGCACACACACCACTTATGG 145
Qy      137 ACAAACTTTTCTGGAAATTTGGCAAAATTTGGNAGCACACGGTCTTCATGTTGGATGTC 196
Db      146 ACAAGCTGTGTTCGGGCAATTTGGGCTCAAAATTTAGGCACATGGTCTTCATGTTGGTCTCC 205
Qy      197 CAGAAGGCTTAATGGGAAATTTCTGAAGTTGGACATTTTGAATATAGGAGCTGGAAGAGCTTA 256
Db      206 CAGNAGGATGATGGGAAATTCGGAAGTCGACATTTTGACATCGGACCGGACGCTGTTA 265
Qy      257 TTTATCAAGATATTGTTCGAATTAATTTGCGTTTCAACGAAACAGAGTCTTGTTCACAAATC 316
Db      266 TCTATCAAGACATTTGTCGTATTAACTCTGCAGTCACAGAACACAAATTTGTGACTAATG 325

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QY 317 CTCAGATTGTTGCATCAGCTGACGCTGCAAGAGGAGGAGTGTGCTGATTCATTATTAG 376
 DB 326 AGAGCTTGGTGGATGCTTGGATGCTGCTAAACCGAATGACGCTTCATCTCGCCG 385
 QY 377 GACTGTTAGCGATGTTGGTGTCCACTCTCATATTGATCATCTTTTGGCTTGTATACGTTG 436
 DB 386 GACTTGTCTGACGAGGTGTTCAATCTCATATTGATCATCATGTTTGTGTTAAAG 445
 QY 437 CATTAAACAATTAACAAGTGCACAAAGTTTTCATTTCACATTTTGTGCTGTCGAGATA 496
 DB 446 CCATCAAGAGCTGCGAGTTCAGAACTTTACCTTCTATTCACGAGATGTCGTGATA 505
 QY 497 CTTGCGCAACAAGTGGAGTGTATCTTGAACAACCTTCTCAATTTATTG---CTTCGG 553
 DB 506 CTTCTCCAAACAGTGGAGTGGATCTTGAACAACCCCTCGAGTTCCTGGAGAAACTA 565
 QY 554 AAAAGTACGAGAAATTTGGCTACTATTACTGAGGCTTATTATGCAATGATAGGACAAA 613
 DB 566 CTGGATATGAAAACCTAGCTACTGTAGTTGGCGCTACTATGCTATGATGCGGATAACA 625
 QY 614 GATGGAGCGCTATTAGATGGCTTATG 640
 DB 626 GATGGAGCGCTATCAATGTGCATACG 652

RESULT 8

BJ108160

LOCUS

DEFINITION BJ108160 649 bp mRNA linear EST 23-JAN-2002
 Caenorhabditis elegans cDNA library, C. elegans L1 stage

ACCESSION

BJ108160

VERSION

1

KEYWORDS

EST.

SOURCE

Caenorhabditis elegans

ORGANISM

Caenorhabditis elegans

REFERENCE

1

AUTHORS

Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.

TITLE

A complementary view of the C.elegans genome

JOURNAL

Unpublished

COMMENT

Contact: Tadasu Shin-I

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. .649

/organism="Caenorhabditis elegans"

/mol_type="mRNA"

/strain="N2"

/db_xref="taxon:6239"

/clone="yk1104f08"

/sex="hermaphrodite"

/tissue_type="whole animal"

/dev_stage="L1"

/clone_lib="unpublished oligo-capped cDNA library, C.

elegans L1 stage"

BASE COUNT 174 a 124 c 165 g 186 t

ORIGIN

Query Match

Best Local Similarity 16.7%; Score 287.6; DB 12; Length 649;

Matches 421; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

QY 17 TTGAGATGGACAAATATCAAAATGTTCAACAAAAGTCTGCTGTAGTTATTGATGGAT 76

DB 24 TGGCGATGCAAAATACAGTTGGTGGCGCAATAGTCTGCTCATCTATTGATGGAT 83

QY 77 GGGCGCTTTCCGATGAACACACGCGGAATGCAATTCGTAAGCTAAAGCTAAAGCCCTATTATGG 136
 DB 84 GGGGAGTTTCTGNAGATCCCTTACGGTAAACGCTATTCACACGACACAGACACCACTTATGG 143
 QY 137 ACAAACTTTGTTCTTGGAAATTTGGCAAAAATTTGGAAGCACACGCTCTTCATGTTGGATTGC 196
 DB 144 ACAAGCTGTGTTGGGCAATTTGGGCTCAAAATTTGAGGCACATGCTCTTCATGTTGGTCTCC 203
 QY 197 CAGAAGCTTAATGGGAAATTTCTGAAGTTGGACATTTGAATATAGAGAGTGGAGAGTTA 256
 DB 204 CAGAAGATTTGATGGGAAATTTGGAAATCGGACATTTGAACATCGGAGCGGACGTTGTTA 263
 QY 257 TTTATCAACATATTTGTCGAATTAATTTGGCTGTTTCAAGGAAACGAGTTTGTATACAAATC 316
 DB 264 TCTATCAACACATTTGTCGATTAATTTGCGAGTCAAGAACACAAATTTGTGACCTAATG 323
 QY 317 CTCAGATTTGTCATCAGCTGAGCGTGCACAAAGAGGGAGTGTGCTGATTCGATTTATTTAG 376
 DB 324 AGAGCTTGTGGATGCTTGGATCGTGTCTAAACGGAATGACGCTCTCATCTGCGCG 383
 QY 377 GACTGTTAGCGATGCTGCTCCACTCTCATATTGATCATCTTTTGGTGTGATACGTG 436
 DB 384 GACTTGTCTGACGAGGTGTTCAATTCATATTGATCATGTTTGTGTTGTTAAAG 443
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RESULT 9

CB374256

LOCUS

DEFINITION

ro99h09.y1.Heterodera glycines J3 Heterodera glycines cDNA 5',

similar to TR:O44742 O44742 F57B10.3 PROTEIN. [1] ; mRNA sequence.

CB374256

ACCESSION

CB374256.1

VERSION

GI:29049477

KEYWORDS

EST.

SOURCE

Heterodera glycines

ORGANISM

Heterodera glycines

REFERENCE

1

AUTHORS

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,

Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R.,

Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Septoe,

M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,

Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and

Wilson, R.

TITLE

The Washington Univ. Nematode EST Project, 1999

JOURNAL

Unpublished

COMMENT

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This library was generated by cloning cDNAs directionally into

Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and 77/XhoI

are at the 3'-end). The library was excised [now in plasmid]

SK(+)] and normalized (Bonardo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcderm@iastate.edu).

Seq primer: T3 from Gibco
High quality sequence stop: 469.

FEATURES

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1. 647
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/note=Vector: pBluescript SK+ (Stratagene); Site_1: XhoI; Site_2: EcoRI; This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised [now in pBluescript SK(+)] and normalized (Bonardo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jpmcderm@iastate.edu)."
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601 AAGAACGCGAGTTGGTCCCATCGCGA 627
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LOCUS
DEFINITION
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incognita cDNA 5' similar to TR:044742 044742 F57B10.3 PROTEIN. [1]
; mRNA sequence.
BQ613449
VERSION BQ613449.1 GI:21603118
KEYWORDS
SOURCE EST.
ORGANISM
Meloiodogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Meloiodogyninae; Meloiodogyne.
1 (bases 1 to 285)
McCartier,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarelshvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,
M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished
Contact: McCartier JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. Meloiodogyne incognita eggs
were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
Putative full length read
The vector to vector length is 286
Seq primer: -408P from Gibco.
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Site_2: EcoRI; The library was constructed by Claire
Murphy and Dr. James McCarter at Washington University,
St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR
products of size >400 nucleotides containing SL1 on the 5'
end and oligo(dT) on the 3' end were non-directionally
cloned into pCR11-TOPO(Invitrogen) following the TOPO TA
cloning protocol. Meloiodogyne incognita eggs were provided
by Andrew Kloek of Divergence Inc., St. Louis, MO."
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Db 62 ATTATGACAACTTTTGTCTGGAAATTTGGCAAAATTTGGAAGCACACGCTTCTCATGTT 121
Qy 190 GGATTGCCAAGAGCGCTTAATGGAAATTTCTGAAGTTGGACATTTTGAATATAGGAGCTGGA 249


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RESULT 13
BJ107756
LOCUS
DEFINITION
BJ107756 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1100b08 5', mRNA sequence.
BJ107756
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 620)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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BJ155870 unpublished oligo-capped cDNA library, C. elegans L1 stage
Caenorhabditis elegans cDNA clone yk1347c03 3', mRNA sequence.
BJ155870
VERSION
KEYWORDS
SOURCE
ORGANISM
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 726)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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FEATURES
source
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Caenorhabditis elegans cDNA clone yk1219f08 5', mRNA sequence.
ACCESSION
BJ117851
VERSION
EST.
KEYWORDS
Caenorhabditis elegans

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ORGANISM      Caenorhabditis elegans
REFERENCE      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
AUTHORS        1 (bases 1 to 621)
                Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
                and Sugano,S.
TITLE          A complementary view of the C.elegans genome
JOURNAL        Unpublished
COMMENT        Contact: Tadasu Shin-i
                Center For Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6856
                Fax: 81-559-81-6855
                Email: tshinigenes.nig.ac.jp.
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Best Local Similarity 68.5%; Pred. No. 1.1e-54;
Matches 387; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

QY 47 AAAAACTGCTCTGTAGTTATGATGGGCTTTCGATGAACACACGGAATG 106
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QY 287 CTGTTCAAGCAACAGATTTGTTACAAATCCTCAGATTTCTCATCAGCTGAGCGTGCAA 346
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Db 476 ACCTTCATTTTACCGAGATGCTGCTGATCTTCTCCAAACAGTGGAGTGTGATTCCTTG 535
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Mon Aug 4 16:18:14 2003

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Page 11

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